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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/614,599	07/07/2003	David P. Andrew	09800080-0104	7759

23552 7590 10/29/2007

MERCHANT & GOULD PC
P.O. BOX 2903
MINNEAPOLIS, MN 55402-0903

EXAMINER	
DEBERRY, REGINA M	
ART UNIT	**PAPER NUMBER**
1647	

MAIL DATE	DELIVERY MODE
10/29/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/614,599	ANDREW ET AL.	
	Examiner	Art Unit	
	Regina M. DeBerry	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *27 August 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *19,38,42-48,51-57,61-64 and 66-75* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *19,38,42-48,51-57,61-64 and 66-75* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *8/07*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

Continued Examination Under 37 CFR 1.114

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 27 August 2007 has been entered.

Status of Application, Amendments and/or Claims

The amendment filed 27 August 2007 has been entered in full. Claims 1-18, 20-37, 39-41, 49, 50, 58-60, 65 are canceled. Claims 19, 38, 42-48, 51-57, 61-64, 66-75 are pending and under examination.

Information Disclosure Statement

The information disclosure statement(s)(IDS) filed 27 August 2007 was received and complies with the provisions of 37 CFR §§1.97 and 1.98. It has been placed in the application file and the information referred to therein has been considered as to the merits.

Withdrawn Objections And/Or Rejections

The rejection to claims 19, 38, 42-60 under 35 U.S.C. 112, first paragraph, written description, as set forth at pages 8-10 of the previous Office Action (02 February 2007), is *withdrawn* in view of the amendment (27 August 2007).

The objection to claims 19, 38 and 59, as set forth at page 10 of the previous Office Action (02 February 2007), is *withdrawn* in view of the amendment (27 August 2007).

The rejection to claims 19, 42-50 under 35 U.S.C. 112, second paragraph, as set forth at page 10 of the previous Office Action (02 February 2007), is *withdrawn* in view of the amendment (27 August 2007).

Claim Rejections - 35 USC § 112, First Paragraph

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 19, 38, 42-48, 51-57, 61-64, 66-75 remain rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The basis for this rejection is set forth at pages 3-8 of the previous Office Action (02 February 2007).

Applicant states that the Office Action alleges the tumor marker data provided in the specification does not enable the full scope of the claims. Applicant states that the Examiner alleges it is unclear if the nucleic acid levels are enhanced or decreased compared to normal control tissues because of inconsistent expression of the nucleic acid molecules in the same tissues and concludes it is not clear which samples are

statistically significant. Applicant submits that the Examiner is requiring Applicants to establish enablement to a higher degree of certainty than is required. An enabling disclosure only requires a reasonable correlation to the scope of the claims and that as long as the specification discloses at least one method for making and using the claimed invention that bears a reasonable correlation to the entire scope of the claim, then the enablement requirement is satisfied *(In re Fischer,* 427 F.2d 833, 839(CCPA 1970)). For a claimed genus, representative examples coupled with a statement applicable to the genus as a whole are ordinarily sufficient to comply with the enablement requirement (MPEP § 2164.02). Applicant argues that the claims have been amended to recite detecting an alteration in expression of the nucleic acid molecules in a tumor cell compared to a normal cell. Applicant argues that Table 8 shows expression of the nucleic acid molecules is altered in pancreas, liver, colon, stomach, thyroid, kidney, and bladder cancer cells relative to normal cells from the respective tissues. Table 9 shows expression of the nucleic acid molecules in tumor tissue compared to normal adjacent tissue in the same patient or normal tissue from a different patient. Applicant argues that in some instances, expression of the nucleic acid molecules is increased relative to the control (see, for example, colon and liver in Tables 8 and 9) and that in some instances, expression of the nucleic acid molecules is decreased relative to the control (see, for example, kidney and prostate). Applicant maintains that an increase or decrease in expression of the nucleic acid molecules in tumor cells or tumor tissue relative to the control cells or control tissue was indicative of cancer. Applicant submits the data provide in Tables 8 and 9 provide a reasonable

correlation between an alteration in expression of the nucleic acid molecules in the recited cells and tissues and cancer. Applicant states that contrary to the Examiner's assertion, Tables 8 and 9 provide a control cell or control tissue for each cell type or tissue type and that post filing date information, indicates that the polypeptide comprising SEQ ID NO:6 has been categorized as S100 protein A14. Applicant submits an alignment. Applicant states that members of the S100 family have been implicated as markers for cancer tissue. Applicant state that with respect to the results presented in the application for breast, prostate, and colon cancer, analysis of circulating tumor cells indicates that S100A14 serves as a marker for breast cancer and colon cancer cells. Applicant cites Smirnov et al. (Cancer Res.65:4993, 2006).

Applicant's arguments have been fully considered but are not deemed persuasive. The instant claims remain rejected because the specification was not enabling as of the filing date (18 November 1999; filing date of the instant application). That is to say that the specification failed to teach how to use the instant invention of determining cancer of the pancreas, liver, colon, thyroid, kidney or bladder at the time of filing. The Examiner has cited some of the teachings from MPEP 2164.05 (a) [R-2]. "The state of the art for a given technology is not static in time. It is entirely possible that a disclosure filed on January 2, 1990, would not have been enabled. However, if the same disclosure had been filed on January 2, 1996, it might have enabled the claims. Therefore, the state of the prior art must be evaluated for each application based on its filing date. Publications dated after the filing date providing information publicly first disclosed after the filing date generally cannot be used to show what was known at the

time of filing. In re Gunn, 537 F.2d 1123, 1128, 190 USPQ 402,405-06 (CCPA 1976); In re Budnick, 537 F.2d 535, 538, 190 USPQ 422, 424 (CCPA 1976). While a later dated publication cannot supplement an insufficient disclosure in a prior dated application to make it enabling, Applicant can offer the testimony of an expert based on the publication as evidence of the level of skill in the art at the time the application was filed. Gould v. Quigg, 822 F.2d 1074, 1077, 3 USPQ2d 1302, 1304 (Fed. Cir. 1987)".

Applicant argues that the claims have been amended to recite detecting an alteration in expression of the nucleic acid molecules in a tumor cell compared to a normal cell. This argument is not found persuasive. If one skilled in the art had a sample of normal tissue and possible cancerous tissue, what type of alteration would the skilled artisan be looking for? Does alteration mean overexpression or underexpression? It is unclear how the limitation "altered" enables one skilled in the art to discern cancer in a particular type of tissue. Botsein et al., US Patent 7,157,247 B2, for example, teach a **gene that is amplified** in certain cancer or cancer cell lines (column 547-561). The skilled artisan would know to look for an overexpression of the gene of Botsein et al. in cancer samples. Applicant cites Smirnov et al. (Cancer Res.65:4993, 2006) and argues that with respect to the results presented in the application for breast, prostate, and colon cancer, analysis of circulating tumor cells indicates that S100A14 serves as a marker for breast cancer and colon cancer cells. The Examiner does not doubt that S100A14 can serve as a marker for certain cancers based on Smirnov et al. But, publications dated after the filing date providing information publicly first disclosed after the filing date generally cannot be used to show what was known at the time of filing.

Applicant argues that in some instances, expression of the nucleic acid molecules is increased relative to the control (for example, colon and liver in Tables 8 and 9) and that in some instances, expression of the nucleic acid molecules is decreased relative to the control (for example, kidney and prostate). This argument is not found persuasive. The specification teaches the quantitative expression of SEQ ID NO:5 in various tissue. The specification teaches normal kidney tissue with an SEQ ID NO:5 expression level of 4.6 and renal carcinomas with numbers of 0.1 (Table 8). Normal kidney tissue from surgical tissue had a SEQ ID NO:5 expression number of 2.9, surgical kidney cancers had numbers of 2.4 (Table 9, page 91). However, the specification states that the results in Table 8 indicate that the clone of SEQ ID NO:5 is very strongly expressed in several tumor derived cell lines compared with normal tissue (see page 88, lines 1-10 and page 91, lines 1-8). This is an example of an inconsistency because the gene appears to be underexpressed in kidney, but the summary of the data teaches that SEQ ID NO:5 is strongly expressed. It is unclear how one skilled in the art can use this particular teaching. The specification teaches normal colorectal tissue with a SEQ ID NO:5 expression level of 3.6 (page 87) and colon carcinomas with levels of 0.3, 4.3, 12.0, 31.4, 44.2 and 100 (page 88). Surgical normal colon tissue had a SEQ ID NO:5 expression level of 22.4, CC Well to Mod Diff had a level of 32, CC NAT had a level of 11.5, CC NAT had a level of 2.7, CC Mod Diff had a level of 5.7, CC NAT had a level of 5.2, CC NAT had a level of 10.8 (page 90). This is another example of an inconsistency because it is not clear if this gene is overexpressed or underexpressed in colon cancer compared to normal colon tissue. The Examiner suggested in a phone interview (27

August 2007) that Applicant provide teachings (e.g. literature, declarations, etc), which would explain the inconsistencies in the data and why the data is still statistically relevant. The literature and arguments submitted by Applicant fail to address the instant issues. Applicant maintains that an increase or decrease in expression of the nucleic acid molecules in tumor cells or tumor tissue relative to the control cells or control tissue is indicative of cancer. However, this is not necessarily clear from the instant data and the instant claims fail to recite such limitations.

The scientific reasoning and evidence as a whole indicates that the rejection should be maintained.

NEW CLAIM REJECTIONS/OBJECTIONS

Claim Rejections-35 USC § 112, First Paragraph, Written Description (New Matter)

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 19, 42-48 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. **This is a new matter rejection.**

The specification as originally filed does not provide support for the invention as now claimed: "detecting an amount of said nucleic acid molecule in said sample,

wherein a change in expression as compared to normal cells of the same tissue type is indicative of cancer". Applicant's amendment, filed 27 August 2007, states that the claims have been amended to further clarify the claimed invention.

The Examiner cannot locate support for the deletion of "enhanced" in the limitation, "..wherein a change in enhanced expression of the nucleic acid molecule..". The wording or connotation of the instant claim(s) is not readily apparent and Applicant does not provide sufficient direction for the written description for the above-mentioned "limitations".

Furthermore, the specification teaches that, "the results in Table 8 indicate that the clone of SEQ ID NO:5 is very strongly expressed in several tumor derived cell lines compare with normal tissue, especially colon tumor cells, breast tumor cells and ovarian tumor cells" (page 88, lines 4-7). The specification also states, "the results shown in Table 9 demonstrate that 65677221-3 frag is strongly upregulated by cancer cell lines and tumor, compared to normal and normal adjacent tissue". "This is especially true for cancers of the breast, ovary, colon, stomach and pancreas" (page 91, lines 2-6).

The specification as filed does not provide a written description or set forth the metes and bounds of this "limitations". The instant claims now recite limitations which were not clearly disclosed in the specification as filed, and now change the scope of the instant disclosure as-filed. Applicant is required to cancel the new matter in the response to this Office action. Alternatively, Applicant is invited to provide specific written support for the "limitations" indicated above or rely upon the limitations set forth in the specification as filed.

Art of Record

The art made of record and not relied upon is considered pertinent to Applicant's disclosure are WO document, WO 99/47669 and foreign document, DE 198 13 839 A1. The instant references teach the polynucleotide sequence which is 100% identical to a polynucleotide sequence encoding instant SEQ ID NO:6. See Appendix A, result #7 and Appendix B, result #6. The instant documents identify their sequence as encoding a calcium binding protein. However the instant references teach that their nucleic acid sequence can be used to identify breast cancer and thus cannot be considered prior art because the instant claims recite a method for detecting cancer using a nucleic acid encoding the amino acid of SEQ ID NO:6 in pancreas, liver, colon, thyroid, kidney or bladder cancer cells.

The art made of record and not relied upon is considered pertinent to Applicant's disclosure is Pietas et al. (Molecular cloning and characterization of the human S100A14 gene encoding a novel member of the S100 family; Genomics, Vol. 79, No. 4, April 2002). The instant references teach the polynucleotide sequence which is 100% identical to a polynucleotide sequence encoding instant SEQ ID NO:6. See Appendix B, result #4. Pietas et al. teach the heterogenic expression of S100A14 in tumors, demonstrating its overexpression in breast and underexpression in kidney. However the instant reference has a publication date of April 2002 and thus cannot be considered prior art.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Regina M. DeBerry whose telephone number is (571) 272-0882. The examiner can normally be reached on 9:00 a.m.-6:30 p.m.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Manjunath N. Rao can be reached on (571) 272-0939. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

RMD
10/23/07

Marianne P. Allen
MARIANNE P. ALLEN
PRIMARY EXAMINER
AU 1647 10/26/07

Appendix A

SCORE Search Results Details for Application 10614599 and Search Result us-10-614-599-6.p2n.rng.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10614599 and Search Result us-10-614-599-6.p2n.rng.

Go Back to previous page

```
                          GenCore version 5.1.9
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:          July 12, 2006, 21:14:05 ; Search time 376.273 Seconds
                                            (without alignments)
                                            3279.767 Million cell updates/sec

Title:           US-10-614-599-6
Perfect score:   614
Sequence:        1 DNRTLTKGPDTVSTMGQCRS.........WELIGEAAKSVKLERPVRGH 118

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10614599/runat_12072006_133551_22754/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10614599_@CGN_1_1_1423_@runat_12072006_133551_22754 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       N_Geneseq_8:*
                 1:  geneseqn1980s:*
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                 9:  geneseqn2003bs:*
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                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
                 14:  geneseqn2005s:*
                 15:  geneseqn2006s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                 %
```

Appendix A

	Result No.	Score	Query Match	Length	DB	ID	Description
c	1	614	100.0	379	5	AAS00674	Aas00674 Human con
	2	614	100.0	1026	14	AED26049	Aed26049 Novel hum
	3	614	100.0	1057	8	ACC50213	Acc50213 Breast ca
	4	614	100.0	1057	12	ADN04843	Adn04843 Antipsori
	5	614	100.0	1057	13	ADX97504	Adx97504 Pancreati
	6	614	100.0	1057	14	AEB35221	Aeb35221 Human Gef
	7	614	100.0	1105	2	AAZ33627	Aaz33627 Human bre
	8	610	99.3	437	5	AAF68153	Aaf68153 Human lun
	9	610	99.3	437	6	ABK38064	Abk38064 cDNA enco
	10	610	99.3	437	8	ACA10393	Aca10393 Human lun
	11	610	99.3	437	8	ABX99344	Abx99344 Lung canc
	12	610	99.3	437	10	ADH45590	Adh45590 Human lun
	13	610	99.3	437	12	ADE72127	Ade72127 Human lun
	14	610	99.3	437	13	ADJ19509	Adj19509 Human lun
	15	610	99.3	489	14	AEA36199	Aea36199 Human nuc
	16	610	99.3	1063	3	AAF21843	Aaf21843 Human bre
	17	610	99.3	1202	5	ADL62099	Adl62099 Human ova
	18	610	99.3	1299	8	ABX77589	Abx77589 Different
	19	610	99.3	1299	9	ACH04218	Ach04218 Human cDN
	20	602	98.0	491	4	AAH99905	Aah99905 Nucleotid
	21	602	98.0	491	5	AAS43039	Aas43039 Breast ca
	22	602	98.0	491	12	ADJ99969	Adj99969 Breast ca
	23	591	96.3	1065	14	AED26341	Aed26341 Novel hum
	24	587	95.6	357	5	AAS00673	Aas00673 Human exp
	25	556	90.6	405	13	ADR59898	Adr59898 Cotton cD
	26	542	88.3	436	6	ABK53972	Abk53972 Human hea
	27	505.5	82.3	1670	5	AAS00672	Aas00672 Murine cy
	28	454	73.9	326	6	ABK53939	Abk53939 Human hea
c	29	357	58.1	1299	8	ABX77589	Abx77589 Different
c	30	357	58.1	1299	9	ACH04218	Ach04218 Human cDN
	31	331	53.9	212	5	AAS00671	Aas00671 Murine cy
	32	326	53.1	700	10	ACD92384	Acd92384 Human col
	33	309	50.3	277	2	AAT26829	Aat26829 Human gen
c	34	256	41.7	231	6	ABV97049	Abv97049 Human pan
	35	254	41.4	385	4	AAS37473	Aas37473 Novel hum
c	36	235	38.3	256	5	ADI75725	Adi75725 Human ova
c	37	235	38.3	256	5	ADI69383	Adi69383 Human ova
c	38	235	38.3	551	5	ADL40961	Adl40961 Human ova
	39	224	36.5	577	6	ABQ56600	Abq56600 Human col
	40	189	30.8	418	4	AAS37336	Aas37336 Novel hum
	41	184.5	30.0	297	3	AAC81813	Aac81813 Human S10
	42	184.5	30.0	470	14	ACL54499	Acl54499 Human col
	43	184.5	30.0	480	8	ABZ34794	Abz34794 Coding se
	44	184.5	30.0	481	6	ABL67535	Abl67535 Thyroid c
	45	184.5	30.0	481	6	ABN97345	Abn97345 Gene #384

ALIGNMENTS

```
RESULT 1
AAS00674/c
ID   AAS00674 standard; DNA; 379 BP.
XX
AC   AAS00674;
XX
DT   07-SEP-2001  (first entry)
XX
DE   Human consensus sequence 65677221-3-frag DNA.
XX
KW   Wnt signalling pathway; FCTRX; cytokine-like polypeptide; human; cancer;
KW   immune system disorder; tissue proliferation; neurological disorder; ds;
KW   septic shock; arthritis; Crohn's disease; anaphylaxis; haemophilia; EST;
KW   stroke; inflammatory bowel disease; depressive disorder; mammary tumour;
KW   cognitive disorder; psoriasis; clone 7971c.7; expressed sequence tag;
KW   consensus sequence 65677221-3-frag.
XX
OS   Homo sapiens.
XX
PN   WO200136644-A2.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031629.
XX
PR   18-NOV-1999;   99US-0166177P.
PR   16-NOV-2000; 2000US-00166177.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Rastelli L,  Lewin D,  Taillon B,  Andrew DP;
XX
DR   WPI; 2001-329224/34.
DR   P-PSDB; AAU00682.
XX
PT   S100 cytokine-like polypeptide member of the Wnt signaling pathway
PT   designated (FCTRX) and the nucleic acid that encodes it, useful for
PT   preventing, diagnosing and treating e.g. cancers and inflammation.
XX
```

Appendix A

```
Score:                  614.00          Matches:        118
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     14              Gaps:           0

US-10-614-599-6 (1-118) x AEB35221 (1-1057)

Qy          1 AspAsnArgThrLeuThrLysGlyProAspThrValSerThrMetGlyGlnCysArgSer 20
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Qy         21 AlaAsnAlaGluAspAlaGlnGluPheSerAspValGluArgAlaIleGluThrLeuIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         41 LysAsnPheHisGlnTyrSerValGluGlyGlyLysGluThrLeuThrProSerGluLeu 60
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Db        177 AAGAACTTTCACCAGTACTCCGTGGAGGGTGGGAAGGAGACGCTGACCCCTTCTGAGCTA 236

Qy         61 ArgAspLeuValThrGlnGlnLeuProHisLeuMetProSerAsnCysGlyLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 CGGGACCTGGTCACCCAGCAGCTGCCCCATCTCATGCCGAGCAACTGTGGCCTGGAAGAG 296

Qy         81 LysIleAlaAsnLeuGlySerCysAsnAspSerLysLeuGluPheArgSerPheTrpGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 AAAATTGCCAACCTGGGCAGCTGCAATGACTCTAAACTGGAGTTCAGGAGTTTCTGGGAG 356

Qy        101 LeuIleGlyGluAlaAlaLysSerValLysLeuGluArgProValArgGlyHis 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 CTGATTGGAGAAGCGGCCAAGAGTGTGAAGCTGGAGAGGCCTGTCCGGGGGCAC 410

RESULT 7
AAZ33627
ID   AAZ33627 standard; cDNA; 1105 BP.
XX
AC   AAZ33627;
XX
DT   08-DEC-1999  (first entry)
XX
DE   Human breast tumour-associated EST 17.
XX
KW   Expressed sequence tag; EST; human; breast; cancer; gene therapy;
KW   treatment; tumour; cytostatic; medicament; ss.
XX
OS   Homo sapiens.
XX
PN   DE19813839-A1.
XX
PD   23-SEP-1999.
XX
PF   20-MAR-1998;   98DE-01013839.
XX
PR   20-MAR-1998;   98DE-01013839.
XX
PA   (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI   Specht T,  Hinzmann B,  Schmitt A,  Pilarsky C,  Dahl E,  Rosentahl A;
XX
DR   WPI; 1999-528981/45.
XX
PT   Human nucleic acid sequences and protein products from tumor breast
PT   tissue, useful for breast cancer therapy.
XX
PS   Claim 1a; 97; 188pp; German.
XX
CC   This invention decribes novel human nucleic acid sequences from tumor
CC   breast tissue which have cytostatic activity. The nucleic acid sequences
CC   can be used to produce and isolate full-length gene sequences. They can
CC   be used to express proteins, which can be used as tools to find an
CC   activity against breast cancer. The sequences can be used in sense or
CC   antisense form. They are especially useful for medicaments for gene
CC   therapy to treat breast cancer. AAZ33611-Z48617 represents expressed
CC   sequence tags described in the method of the invention
XX
SQ   Sequence 1105 BP; 256 A; 270 C; 334 G; 245 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.07e-69        Length:         1105
Score:                  614.00          Matches:        118
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-614-599-6 (1-118) x AAZ33627 (1-1105)

Qy          1 AspAsnArgThrLeuThrLysGlyProAspThrValSerThrMetGlyGlnCysArgSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 GACAACAGAACTCTCACCAAAGGACCAGACACAGTGAGCACCATGGGACAGTGTCGGTCA 197
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Appendix A

```
Qy         21 AlaAsnAlaGluAspAlaGlnGluPheSerAspValGluArgAlaIleGluThrLeuIle 40
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Db        198 GCCAACGCAGAGGATGCTCAGGAATTCAGTGATGTGGAGAGGGCCATTGAGACCCTCATC 257

Qy         41 LysAsnPheHisGlnTyrSerValGluGlyGlyLysGluThrLeuThrProSerGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 AAGAACTTTCACCAGTACTCCGTGGAGGGTGGGAAGGAGACGCTGACCCCTTCTGAGCTA 317

Qy         61 ArgAspLeuValThrGlnGlnLeuProHisLeuMetProSerAsnCysGlyLeuGluGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 CGGGACCTGGTCACCCAGCAGCTGCCCCATCTCATGCCGAGCAACTGTGGCCTGGAAGAG 377

Qy         81 LysIleAlaAsnLeuGlySerCysAsnAspSerLysLeuGluPheArgSerPheTrpGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 AAAATTGCCAACCTGGGCAGCTGCAATGACTCTAAACTGGAGTTCAGGAGTTTCTGGGAG 437

Qy        101 LeuIleGlyGluAlaAlaLysSerValLysLeuGluArgProValArgGlyHis 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 CTGATTGGAGAAGCGGCCAAGAGTGTGAAGCTGGAGAGGCCTGTCCGGGGGCAC 491

RESULT 8
AAF68153
ID   AAF68153 standard; cDNA; 437 BP.
XX
AC   AAF68153;
XX
DT   12-APR-2001  (first entry)
XX
DE   Human lung tumour protein related nucleotide sequence SEQ ID NO:71.
XX
KW   Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW   lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW   cytostatic; antisense inhibition; ss.
XX
OS   Homo sapiens.
XX
PN   WO200100828-A2.
XX
PD   04-JAN-2001.
XX
PF   30-JUN-2000; 2000WO-US018061.
XX
PR   30-JUN-1999;   99US-00346492.
PR   15-OCT-1999;   99US-00419356.
PR   17-DEC-1999;   99US-00466867.
PR   30-DEC-1999;   99US-00476300.
PR   06-MAR-2000; 2000US-00519642.
PR   22-MAR-2000; 2000US-00533077.
PR   10-APR-2000; 2000US-00546259.
PR   27-APR-2000; 2000US-00560406.
PR   05-JUN-2000; 2000US-00589184.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Wang T,  Bangur CS,  Lodes MJ,  Fanger GR,  Vedvick TS,  Carter D;
PI   Retter MW,  Mannion J;
XX
DR   WPI; 2001-071488/08.
XX
PT   Lung tumor-associated proteins and the nucleic acids that encode them,
PT   useful for preventing, diagnosing and treating lung cancer.
XX
PS   Claim 4; Page 174; 436pp; English.
XX
CC   The present invention describes immunogenic portions of lung tumour-
CC   associated proteins (I) and the nucleic acids (NAs) that encode them. (I)
CC   have cytostatic activity and can be used in gene therapy, antisense
CC   inhibition and in vaccines. The NAs and the lung tumour-associated
CC   proteins they encode may be used in the prevention, treatment and
CC   diagnosis of diseases associated with their inappropriate expression,
CC   especially lung cancers. For example, the NAs may be administered to
CC   treat diseases by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of the protein by expressing inactive proteins
CC   or to supplement the patients own production of (I). Additionally, the
CC   NAs may be used to produce the lung-tumour associated protein, according
CC   to standard recombinant DNA methodology. Conversely, antisense NA
CC   molecules may be administered to down regulate protein expression by
CC   binding with the cells own genes and preventing their expression. The NA
CC   and complementary sequences may also be used as DNA probes in diagnostic
CC   assays to detect and quantitate the presence of similar NA sequences in
CC   samples, and hence which patients may be in need of treatment for lung
CC   cancer. The (I) may be used as antigens in the production of antibodies
CC   and in assays to identify modulators (agonists and antagonists) of the
CC   expression and activity of the protein. AAF68083 to AAF68878 and AAB76848
CC   to AAB76878 represent human lung tumour protein related nucleotide and
CC   protein sequences which are used in the exemplification of the present
CC   invention
XX
SQ   Sequence 437 BP; 109 A; 114 C; 134 G; 79 T; 0 U; 1 Other;

Alignment Scores:
```

Appendix B

SCORE Search Results Details for Application 10614599 and Search Result us-10-614-599-6.p2n.rge.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10614599 and Search Result us-10-614-599-6.p2n.rge.

Go Back to previous page

```
                        GenCore version 5.1.9
                  Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:         July 12, 2006, 21:17:56 ; Search time 2836.74 Seconds
                                          (without alignments)
                                          3990.037 Million cell updates/sec

Title:          US-10-614-599-6
Perfect score:  614
Sequence:       1 DNRTLTKGPDTVSTMGQCRS.........WELIGEAAKSVKLERPVRGH 118

Scoring table:  BLOSUM62
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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10614599/runat_12072006_133553_22765/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10614599_@CGN_1_1_8663_@runat_12072006_133553_22765 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      GenEmbl:*
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                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
                6:  gb_ro:*
                7:  gb_sts:*
                8:  gb_sy:*
                9:  gb_un:*
                10:  gb_vi:*
                11:  gb_ov:*
                12:  gb_htg:*
                13:  gb_in:*
                14:  gb_om:*
                15:  gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
                %
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Appendix B

	Result No.	Score	Query Match	Length	DB	ID	Description
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	2	614	100.0	1026	14	AED26049	Aed26049 Novel hum
	3	614	100.0	1057	8	ACC50213	Acc50213 Breast ca
	4	614	100.0	1057	12	ADN04843	Adn04843 Antipsori
	5	614	100.0	1057	13	ADX97504	Adx97504 Pancreati
	6	614	100.0	1057	14	AEB35221	Aeb35221 Human Gef
	7	614	100.0	1105	2	AAZ33627	Aaz33627 Human bre
	8	610	99.3	437	5	AAF68153	Aaf68153 Human lun
	9	610	99.3	437	6	ABK38064	Abk38064 cDNA enco
	10	610	99.3	437	8	ACA10393	Aca10393 Human lun
	11	610	99.3	437	8	ABX99344	Abx99344 Lung canc
	12	610	99.3	437	10	ADH45590	Adh45590 Human lun
	13	610	99.3	437	12	ADE72127	Ade72127 Human lun
	14	610	99.3	437	13	ADJ19509	Adj19509 Human lun
	15	610	99.3	489	14	AEA36199	Aea36199 Human nuc
	16	610	99.3	1063	3	AAF21843	Aaf21843 Human bre
	17	610	99.3	1202	5	ADL62099	Adl62099 Human ova
	18	610	99.3	1299	8	ABX77589	Abx77589 Different
	19	610	99.3	1299	9	ACH04218	Ach04218 Human cDN
	20	602	98.0	491	4	AAH99905	Aah99905 Nucleotid
	21	602	98.0	491	5	AAS43039	Aas43039 Breast ca
	22	602	98.0	491	12	ADJ99969	Adj99969 Breast ca
	23	591	96.3	1065	14	AED26341	Aed26341 Novel hum
	24	587	95.6	357	5	AAS00673	Aas00673 Human exp
	25	556	90.6	405	13	ADR59898	Adr59898 Cotton cD
	26	542	88.3	436	6	ABK53972	Abk53972 Human hea
	27	505.5	82.3	1670	5	AAS00672	Aas00672 Murine cy
	28	454	73.9	326	6	ABK53939	Abk53939 Human hea
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c	30	357	58.1	1299	9	ACH04218	Ach04218 Human cDN
	31	331	53.9	212	5	AAS00671	Aas00671 Murine cy
	32	326	53.1	700	10	ACD92384	Acd92384 Human col
	33	309	50.3	277	2	AAT26829	Aat26829 Human gen
c	34	256	41.7	231	6	ABV97049	Abv97049 Human pan
	35	254	41.4	385	4	AAS37473	Aas37473 Novel hum
c	36	235	38.3	256	5	ADI75725	Adi75725 Human ova
c	37	235	38.3	256	5	ADI69383	Adi69383 Human ova
c	38	235	38.3	551	5	ADL40961	Adl40961 Human ova
	39	224	36.5	577	6	ABQ56600	Abq56600 Human col
	40	189	30.8	418	4	AAS37336	Aas37336 Novel hum
	41	184.5	30.0	297	3	AAC81813	Aac81813 Human S10
	42	184.5	30.0	470	14	ACL54499	Acl54499 Human col
	43	184.5	30.0	480	8	ABZ34794	Abz34794 Coding se
	44	184.5	30.0	481	6	ABL67535	Abl67535 Thyroid c
	45	184.5	30.0	481	6	ABN97345	Abn97345 Gene #384

ALIGNMENTS

RESULT 1
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ID AAS00674 standard; DNA; 379 BP.
XX
AC AAS00674;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human consensus sequence 65677221-3-frag DNA.
XX
KW Wnt signalling pathway; FCTRX; cytokine-like polypeptide; human; cancer;
KW immune system disorder; tissue proliferation; neurological disorder; ds;
KW septic shock; arthritis; Crohn's disease; anaphylaxis; haemophilia; EST;
KW stroke; inflammatory bowel disease; depressive disorder; mammary tumour;
KW cognitive disorder; psoriasis; clone 7971c.7; expressed sequence tag;
KW consensus sequence 65677221-3-frag.
XX
OS Homo sapiens.
XX
PN WO200136644-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031629.
XX
PR 18-NOV-1999; 99US-0166177P.
PR 16-NOV-2000; 2000US-00166177.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Rastelli L, Lewin D, Taillon B, Andrew DP;
XX
DR WPI; 2001-329224/34.
DR P-PSDB; AAU00682.
XX
PT S100 cytokine-like polypeptide member of the Wnt signaling pathway
PT designated (FCTRX) and the nucleic acid that encodes it, useful for
PT preventing, diagnosing and treating e.g. cancers and inflammation.
XX

Appendix B

```
VERSION     CQ894742.1  GI:55467491
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rosenthal,A.D., Pilarsky,C., Dahl,E., Specht,T., Bruemmendorf,T.,
            Lichtner,R., Staub,E., Roepcke,S. and Li,X.I.
  TITLE     Human nucleic acid sequences expressed in pancreatic carcinomas
  JOURNAL   Patent: EP 1471075-A 52 27-OCT-2004;
            Hinzmann, Bernd (DE); Rosenthal, Andre (DE); Pilarsky, Christian
            (DE); Dahl, Edgar (DE); Specht, Thomas (DE); Lichtner, Rosemarie
            (DE)
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                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
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Score:                  614.00          Matches:        118
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Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-614-599-6 (1-118) x CQ894742 (1-1057)

Qy          1 AspAsnArgThrLeuThrLysGlyProAspThrValSerThrMetGlyGlnCysArgSer 20
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Qy         21 AlaAsnAlaGluAspAlaGlnGluPheSerAspValGluArgAlaIleGluThrLeuIle 40
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Qy         41 LysAsnPheHisGlnTyrSerValGluGlyGlyLysGluThrLeuThrProSerGluLeu 60
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Qy         61 ArgAspLeuValThrGlnGlnLeuProHisLeuMetProSerAsnCysGlyLeuGluGlu 80
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Qy         81 LysIleAlaAsnLeuGlySerCysAsnAspSerLysLeuGluPheArgSerPheTrpGlu 100
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Db        297 AAAATTGCCAACCTGGGCAGCTGCAATGACTCTAAACTGGAGTTCAGGAGTTTCTGGGAG 356

Qy        101 LeuIleGlyGluAlaAlaLysSerValLysLeuGluArgProValArgGlyHis 118
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Db        357 CTGATTGGAGAAGCGGCCAAGAGTGTGAAGCTGGAGAGGCCTGTCCGGGGGCAC 410

RESULT 4
AY007220
LOCUS       AY007220               1057 bp    mRNA    linear   PRI 21-AUG-2000
DEFINITION  Homo sapiens S100-type calcium binding protein A14 mRNA, complete
            cds.
ACCESSION   AY007220
VERSION     AY007220.1  GI:9945039
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1057)
  AUTHORS   Pietas,A., Petersen,I., Schluens,K. and Petersen,S.
  TITLE     Human cDNA of a new member of the S100 protein family which is
            downregulated in lung carcinoma cells
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1057)
  AUTHORS   Pietas,A., Petersen,I., Schluens,K. and Petersen,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-AUG-2000) Institute of Pathology, Charite Hospital,
            Humboldt University, Schumannstrasse 20/21, Berlin 10098, Germany
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             99. .413
                     /note="S114"
                     /codon_start=1
                     /product="S100-type calcium binding protein A14"
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                     /db_xref="GI:9945040"
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Appendix B

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GH"
ORIGIN

Alignment Scores:
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Percent Similarity: 100.0% Conservative: 0
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Query Match: 100.0% Indels: 0
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US-10-614-599-6 (1-118) x AY007220 (1-1057)

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||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 21 AlaAsnAlaGluAspAlaGlnGluPheSerAspValGluArgAlaIleGluThrLeuIle 40
||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 41 LysAsnPheHisGlnTyrSerValGluGlyGlyLysGluThrLeuThrProSerGluLeu 60
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Db 177 AAGAACTTTCACCAGTACTCCGTGGAGGGTGGGAAGGAGACGCTGACCCCTTCTGAGCTA 236

Qy 61 ArgAspLeuValThrGlnGlnLeuProHisLeuMetProSerAsnCysGlyLeuGluGlu 80
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Db 237 CGGGACCTGGTCACCCAGCAGCTGCCCCATCTCATGCCGAGCAACTGTGGCCTGGAAGAG 296

Qy 81 LysIleAlaAsnLeuGlySerCysAsnAspSerLysLeuGluPheArgSerPheTrpGlu 100
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Db 297 AAAATTGCCAACCTGGGCAGCTGCAATGACTCTAAACTGGAGTTCAGGAGTTTCTGGGAG 356

Qy 101 LeuIleGlyGluAlaAlaLysSerValLysLeuGluArgProValArgGlyHis 118
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Db 357 CTGATTGGAGAAGCGGCCAAGAGTGTGAAGCTGGAGAGGCCTGTCCGGGGGCAC 410

RESULT 5
BD134437
LOCUS BD134437 1105 bp DNA linear PAT 18-SEP-2002
DEFINITION Human nucleic acid sequence originating in mammary tumor tissue.
ACCESSION BD134437
VERSION BD134437.1 GI:23229382
KEYWORDS JP 2002506643-A/15.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1105)
AUTHORS Speft,T., Hintzman,B., Armin,S., Pirarski,C., Edgar,D. and
Rosenthal,A.
TITLE Human nucleic acid sequence originating in mammary tumor tissue
JOURNAL Patent: JP 2002506643-A 15 05-MAR-2002;
METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH
COMMENT OS Homo sapiens (human)
PN JP 2002506643-A/15
PD 05-MAR-2002
PF 19-MAR-1999 JP 2000536852
PR 20-MAR-1998 DE 198 13 839.3
PI THOMAS SPEFT,BERND HINTZMAN,SHCMITT ARMIN,CHRISTIAN PIRARSKI,
PI DUHL EDGAR,
PI ANDRE ROSENTHAL
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P35/00,C07K14/47,
PC C07K16/18,
PC C12N1/19,C12N5/10,C12N15/00,A61K37/02,C12N5/00 CC Human
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tissue
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FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
ORIGIN

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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-614-599-6 (1-118) x BD134437 (1-1105)

Qy 1 AspAsnArgThrLeuThrLysGlyProAspThrValSerThrMetGlyGlnCysArgSer 20
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Appendix B

```
Db        138 GACAACAGAACTCTCACCAAAGGACCAGACACAGTGAGCACCATGGGACAGTGTCGGTCA 197

Qy         21 AlaAsnAlaGluAspAlaGlnGluPheSerAspValGluArgAlaIleGluThrLeuIle 40
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Qy         41 LysAsnPheHisGlnTyrSerValGluGlyGlyLysGluThrLeuThrProSerGluLeu 60
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Qy         61 ArgAspLeuValThrGlnGlnLeuProHisLeuMetProSerAsnCysGlyLeuGluGlu 80
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Db        318 CGGGACCTGGTCACCCAGCAGCTGCCCCATCTCATGCCGAGCAACTGTGGCCTGGAAGAG 377

Qy         81 LysIleAlaAsnLeuGlySerCysAsnAspSerLysLeuGluPheArgSerPheTrpGlu 100
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Db        378 AAAATTGCCAACCTGGGCAGCTGCAATGACTCTAAACTGGAGTTCAGGAGTTTCTGGGAG 437

Qy        101 LeuIleGlyGluAlaAlaLysSerValLysLeuGluArgProValArgGlyHis 118
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RESULT 6
AX017266
LOCUS       AX017266               1105 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 17 from Patent WO9947669.
ACCESSION   AX017266
VERSION     AX017266.1  GI:10042184
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
            Pilarsky,C.
  TITLE     Human nucleic acid sequences from tissue of breast tumors
  JOURNAL   Patent: WO 9947669-A 17 23-SEP-1999;
            SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
            BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
            (DE); PILARSKY CHRISTIAN (DE)
FEATURES             Location/Qualifiers
     source          1. .1105
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              5.81e-72        Length:         1105
Score:                  614.00          Matches:        118
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     2               Gaps:           0

US-10-614-599-6 (1-118) x AX017266 (1-1105)

Qy          1 AspAsnArgThrLeuThrLysGlyProAspThrValSerThrMetGlyGlnCysArgSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 GACAACAGAACTCTCACCAAAGGACCAGACACAGTGAGCACCATGGGACAGTGTCGGTCA 197

Qy         21 AlaAsnAlaGluAspAlaGlnGluPheSerAspValGluArgAlaIleGluThrLeuIle 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 GCCAACGCAGAGGATGCTCAGGAATTCAGTGATGTGGAGAGGGCCATTGAGACCCTCATC 257

Qy         41 LysAsnPheHisGlnTyrSerValGluGlyGlyLysGluThrLeuThrProSerGluLeu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 AAGAACTTTCACCAGTACTCCGTGGAGGGTGGGAAGGAGACGCTGACCCCTTCTGAGCTA 317

Qy         61 ArgAspLeuValThrGlnGlnLeuProHisLeuMetProSerAsnCysGlyLeuGluGlu 80
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Db        318 CGGGACCTGGTCACCCAGCAGCTGCCCCATCTCATGCCGAGCAACTGTGGCCTGGAAGAG 377

Qy         81 LysIleAlaAsnLeuGlySerCysAsnAspSerLysLeuGluPheArgSerPheTrpGlu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 AAAATTGCCAACCTGGGCAGCTGCAATGACTCTAAACTGGAGTTCAGGAGTTTCTGGGAG 437

Qy        101 LeuIleGlyGluAlaAlaLysSerValLysLeuGluArgProValArgGlyHis 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 CTGATTGGAGAAGCGGCCAAGAGTGTGAAGCTGGAGAGGCCTGTCCGGGGGCAC 491

RESULT 7
AX524970
LOCUS       AX524970               1105 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 17 from Patent EP1236799.
ACCESSION   AX524970
VERSION     AX524970.1  GI:25170052
KEYWORDS    .
SOURCE      Homo sapiens (human)
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